

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 5, line 5 with the following rewritten paragraph:

FigureFIG. 2 shows the cDNA and deduced amino acid sequences of human *PIN1* and homologies with other WW domain proteins and PPlases. FigureFIG. 2A shows the Pin1 nucleotide sequence (SEQ ID NO: 1) and predicted Pin1-amino acid sequence (SEQ ID NO: 2) (isaa indicated in one-letter code). The fusion points between GAL4 and Pin1 in six different isolated clones were: clone H20 at C-9; clone H16.24 and 38 at G-+3G+13; clones H6 and H36 at C-+5C+15. Underlined residues form a consensus bipartite nuclear localization signal. The N- and C-terminal boxes indicate the WW domain and PPlase domain, respectively. Nucleotide numbers are on the left and amino acid numbers on right. FigureFIG. 2B and 2C-shows alignmentsthe alignment of the WW domain (B) and PPlase Domain (C) in selected proteins (from top to bottom SEQ ID NOs: 8-14). FIG. 2C shows the alignment of the PPlase domain in selected proteins (from top to bottom SEQ ID NOs: 15-21). In FIGs. 2B and 2C, Identicalidentical residues are shown in the bottom-row labeled "Consensus" (SEQ ID NO: 22). Dashes indicate gaps introduced to make the alignment. Cbf2, cell binding factor 2; SC, *S. cerevisiae*; EC, *E. coli*; BS, *B. subtilis*; CJ, *C. jejuni*; AT, *A. thaliana*.